

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 14, 2005, 20:28:47 ; Search time 2320 Seconds
(without alignments)
9189.782 Million cell updates/sec

Title: US-09-976-054-5

Perfect score: 440
Sequence: 1 cgtccgcgcgcgcgcacttc.....ggatmttagataaaant 440

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	125	28.4	993	AK104808	AK104808 Oryza sat
2	125	28.4	1001	AK104107	AK104107 Oryza sat
3	125	28.4	1010	AK073627	AK073627 Oryza sat
4	123.6	28.1	975	AB012046	AB012046 Hordeum v
5	123.2	28.0	845	TAU22442	TAU22442 Triticum ae
6	107.8	24.5	20420	AY661659	AY661659 Sorghum b
7	93	21.1	848	AY324112	AY324112 Brassica
8	92.8	21.1	279	AR247242	AR247242 Sequence
9	91.4	20.8	893	BT012816	BT012816 Lycopersi
10	88.4	20.1	1036	AY084300	AY084300 Arabidops
11	86.6	19.7	729	ATAPRT	X58640 A. thaliana
12	86.6	19.7	811	BT000370	BT000370 Arabidops
13	86.6	19.7	879	AF325045	AF325045 Arabidops
14	86.6	19.7	887	AY128377	AY128377 Arabidops
15	80.2	18.2	806	AK108481	AK108481 Oryza sat
16	80.2	18.2	1122	AY238894	AY238894 Oryza sat
17	80.2	18.2	1122	AK121982	AK121982 Oryza sat
18	77.6	17.6	1202	AY485263	AY485263 Zea mays
19	77	17.5	552	CQ805734	CQ805734 Sequence

20	77	17.5	583	8	BT004412	BT004412 Arabidops
21	77	17.5	846	8	BT002969	BT002969 Arabidops
22	77	17.5	847	8	AY084513	AY084513 Arabidops
23	76.6	17.4	1097	8	AY255503	AY255503 Triticum
24	73	16.6	1038	8	AK070784	AK070784 Oryza sat
25	73	16.6	1065	8	AK069606	AK069606 Oryza sat
26	72.4	16.5	579	8	AY133689	AY133689 Arabidops
27	72.4	16.5	700	8	BT001111	BT001111 Arabidops
28	69	15.7	579	8	BT001122	BT001122 Arabidops
29	69	15.7	727	8	ATAPRT2	X96866 A. thaliana
30	69	15.7	850	8	AY072021	AY072021 Arabidops
31	67	15.2	607	8	BT005077	BT005077 Arabidops
32	67	15.2	995	8	BT004028	BT004028 Arabidops
33	58.4	13.3	110000	1	AE017282_08	Continuation (9 of
34	58	13.2	143895	8	CNS08CD6	AL954852 Oryza sat
35	52.2	11.9	106702	8	ATPFK2	AL033545 Arabidops
36	52.2	11.9	199577	8	ATCHRIV57	AL161557 Arabidops
37	52	11.8	297850	1	AP006577	AP006577 Gloeobact
38	51.8	11.8	346259	1	BX640435	BX640435 Bordetell
39	51.8	11.8	346287	1	BX640450	BX640450 Bordetell
40	51.2	11.6	86209	8	AP004523	AP004523 Lotus cor
41	51.2	11.6	132741	8	CNS08CAA	AL831797 Oryza sat
42	50.2	11.4	10172	1	AE004187	AE004187 Vibrio ch
43	50.2	11.4	346359	1	BX640411	BX640411 Bordetell
44	49.8	11.3	13614	1	AE006072	AE006072 Pasteurel
45	49.8	11.3	190050	1	AL646059	AL646059 Ralstonia

ALIGNMENTS

RESULT 1	AK104808	993 bp	mRNA	linear	PLN 24-JUL-2003
LOCUS	Oryza sativa (japonica cultivar-group)	CDNA clone:001-040-B09, full insert sequence.			
DEFINITION	AK104808				
ACCESSION	AK104808.1	GI:32990017			
VERSION	AK104808.1	GI:32990017			
KEYWORDS	FLI_CDNA; oligo capping.				
SOURCE	Oryza sativa (japonica cultivar-group)				
ORGANISM	Oryza sativa (japonica cultivar-group)				
REFERENCE	1				
AUTHORS	The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team; Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,B., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group; Otono,Y., Murakami,K., Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y., Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M., Naitikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Nikiura,J., Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J., Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN; Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kondo,S., Komno,H., Miyazaki,A., Osato,N., Ota,Y., Saito,R., Sasaki,D., Sato,K., Shibata,K., Shingawa,A., Shiraki,T., Yoshino,M. and Hayashizaki,Y.				
TITLE	Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice				
JOURNAL	Science 301 (5631), 376-379 (2003)				
MEDLINE	22752273				
PUBMED	12869764				
REFERENCES	2 (bases 1 to 993)				
AUTHORS	Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K., Fujimura,T., Fukuda,S., Hasegaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hizamoto,K., Hiraoka,T., Hori,F., Hotta,I., Iida,J., Iida,Y., Ikeda,R., Imamura,K., Imotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I.,				

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OM nucleic - nucleic search, using sw model

Run on: September 14, 2005, 20:31:16 ; Search time 388 Seconds
(without alignments)
6713.109 Million cell updates/sec

Title: US-09-976-054-5
Perfect score: 440
Sequence: 1 cgtccgcgcgcgcgcacttc.....ggaatnntagataaaaaant 440

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	265.8	60.4	462	3 AAC51765	Aac51765 Zea mays
2	225	51.1	455	3 AAC51740	Aac51740 Zea mays
3	118.8	27.0	216	7 ADS65012	Ads65012 Corn seed
4	99.6	22.6	405	3 AAC43563	Aac43563 Zea mays
5	92.8	21.1	279	10 ABX84141	Abx84141 Corn ear-
6	90.4	20.5	380	3 AAA31767	Aaa31767 Plant mic
7	88.4	20.1	1034	3 AAC49172	Aac49172 Arabidops
8	88.4	20.1	1036	3 AAC35980	Aac35980 Arabidops
9	88.2	20.0	729	2 AAQ35208	Aaq35208 Sequence
10	86.8	19.7	1036	3 AAC40946	Aac40946 Arabidops
11	86.6	19.7	821	3 AAC33967	Aac33967 Arabidops
12	85	19.3	780	3 AAC40942	Aac40942 Arabidops
13	85	19.3	821	3 AAC40945	Aac40945 Arabidops
14	77	17.5	552	3 AAC43276	Aac43276 Arabidops
15	77	17.5	552	12 ADN74250	Adn74250 Thale cre
16	77	17.5	847	3 AAC45129	Aac45129 Arabidops
17	72.4	16.5	459	3 AAC46344	Aac46344 Arabidops
18	72.4	16.5	549	3 AAC42993	Aac42993 Arabidops
19	69	15.7	579	3 AAC44711	Aac44711 Arabidops
20	67.8	15.4	372	3 AAC46302	Aac46302 Arabidops

21	67.8	15.4	1337	3 AAC45318	Aac45318 Arabidops
22	67.8	15.4	1348	3 AAC34911	Aac34911 Arabidops
23	65.2	14.8	744	13 ADR61453	Adr61453 Cotton cd
24	63.8	14.5	945	6 ABN98579	Abn98579 Arabidops
25	55.8	12.7	606	13 ACN53687	Acn53687 Cotton an
26	54.4	12.4	543	13 ADT43091	Adt43091 Bacterial
27	52	11.8	522	13 ADS56186	Ads56186 Bacterial
28	51	11.6	510	13 ADS56682	Ads56682 Bacterial
29	48.6	11.0	615	13 ADT45732	Adt45732 Bacterial
30	47.6	10.8	560	13 ADS62393	Ads62393 Bacterial
31	46.8	10.6	558	13 ADS62685	Ads62685 Bacterial
32	46.8	10.6	558	13 ADS59586	Ads59586 Bacterial
33	44.8	10.2	510	13 ADS55671	Ads55671 Bacterial
34	44.4	10.2	516	13 ADS50157	Ads50157 Bacterial
35	44.4	10.1	519	13 ADS47981	Ads47981 Bacterial
36	43.8	10.0	516	13 ADT45092	Adt45092 Bacterial
37	43.6	9.9	376	4 AAK59140	Aak59140 Human imm
38	43.6	9.9	549	10 ADJ62246	Adj62246 P_aerugin
39	43.6	9.9	549	10 ADJ62248	Adj62248 P_aerugin
40	43.6	9.9	714	11 ABD07892	Abd07892 Pseudomon
41	43	9.8	660	11 ACH99807	Ach99807 Klebsiell
42	42.8	9.7	3132	13 ADT05367	Adt05367 Haemophil
43	42.8	9.7	308766	13 ADT05738	Adt05738 Haemophil
44	42.6	9.7	546	13 ADS59951	Ads59951 Bacterial
45	42.4	9.6	552	10 ACF71497	Acf71497 Photorhab

ALIGNMENTS

RESULT 1					
AAC51765					
ID	AAC51765	standard; DNA; 462 BP.			
XX					
AC	AAC51765;				
XX					
DT	18-OCT-2000	(first entry)			
XX					
DE	Zea mays	DNA fragment SEQ ID NO: 69703.			
XX					
KW	Hybridisation assay; genetic mapping; gene expression control;				
KW	protein identification; signal transduction pathway; metabolic; pathway;				
KW	promoter; termination sequence; corn; ss.				
XX					
OS	Zea mays subsp. mays.				
XX					
PN	EP1033405-A2.				
XX					
PD	06-SEP-2000.				
XX					
PF	25-FEB-2000; 2000BP-00301439.				
XX					
PR	25-FEB-1999;	99US-0121825P.			
PR	05-MAR-1999;	99US-0123180P.			
PR	09-MAR-1999;	99US-0123548P.			
PR	23-MAR-1999;	99US-0125788P.			
PR	25-MAR-1999;	99US-0126264P.			
PR	29-MAR-1999;	99US-0126785P.			
PR	01-APR-1999;	99US-0127462P.			
PR	06-APR-1999;	99US-0128234P.			
PR	08-APR-1999;	99US-0128714P.			
PR	16-APR-1999;	99US-0129845P.			
PR	19-APR-1999;	99US-0130077P.			
PR	21-APR-1999;	99US-0130449P.			
PR	23-APR-1999;	99US-0130510P.			
PR	23-APR-1999;	99US-0130891P.			
PR	28-APR-1999;	99US-0131449P.			
PR	30-APR-1999;	99US-0132048P.			
PR	30-APR-1999;	99US-0132407P.			
PR	04-MAY-1999;	99US-0132484P.			
PR	05-MAY-1999;	99US-0132485P.			
PR	06-MAY-1999;	99US-0132486P.			
PR	06-MAY-1999;	99US-0132487P.			

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OM nucleic - nucleic search, using sw model

Run on: September 14, 2005, 20:22:06 ; Search time 494 Seconds
(without alignments)
5849.364 Million cell updates/sec

Title: US-09-976-054-5
Perfect score: 440
Sequence: 1 cgtccgcgcgcgcgcacttc.....gggaattagataaaant 440

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7351250 seqs, 3283620254 residues
Total number of hits satisfying chosen parameters: 14702500

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
- 22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
- 24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	275.6	62.6	992	US-10-425-114-28279	Sequence 28279, A
2	267.6	60.8	961	US-10-425-114-17257	Sequence 17257, A
3	267.6	60.8	1196	US-10-425-115-37779	Sequence 37779, A
4	267.6	60.8	1396	US-10-425-115-37781	Sequence 37781, A
5	267.6	60.8	1711	US-10-425-115-37775	Sequence 37775, A
6	241	54.8	1123	US-10-425-115-37784	Sequence 37784, A
7	231.6	52.6	1247	US-10-425-115-37780	Sequence 37780, A

C	8	230	52.3	1059	20	US-10-425-115-37783	A
9	225.6	51.3	865	18	US-10-425-114-24105	Sequence 24105, A	
10	216.4	49.2	1065	19	US-10-767-701-11748	Sequence 11748, A	
11	209.6	47.6	815	18	US-10-425-114-31609	Sequence 31609, A	
12	208	47.3	809	18	US-10-425-114-20262	Sequence 20262, A	
13	196.4	44.6	300	20	US-10-425-115-75805	Sequence 75805, A	
14	173	39.3	529	20	US-10-425-115-37777	Sequence 37777, A	
15	169.2	38.5	530	20	US-10-425-115-25089	Sequence 25089, A	
16	166.6	37.9	284	20	US-10-425-115-109858	Sequence 109858, A	
17	154.8	35.2	545	20	US-10-425-115-151541	Sequence 151541, A	
18	135.8	30.9	801	18	US-10-425-114-35919	Sequence 35919, A	
19	135.2	30.7	354	20	US-10-425-115-128907	Sequence 128907, A	
20	129.8	29.5	280	20	US-10-425-115-94349	Sequence 94349, A	
21	125	28.4	1207	19	US-10-437-963-37562	Sequence 37562, A	
22	120.8	27.5	251	20	US-10-425-115-19459	Sequence 19459, A	
23	118.8	27.0	216	9	US-09-923-876-28	Sequence 28, Appl	
24	118.8	27.0	216	10	US-09-923-876-28	Sequence 28, Appl	
25	115.4	26.2	232	20	US-10-425-115-75455	Sequence 75455, A	
26	114.6	26.0	194	20	US-10-425-115-43553	Sequence 43553, A	
27	108.6	24.7	287	20	US-10-425-115-64545	Sequence 64545, A	
28	102.6	23.3	888	18	US-10-424-599-24935	Sequence 24935, A	
29	102.6	23.3	1002	18	US-10-425-114-10919	Sequence 10919, A	
30	102.6	23.3	1182	18	US-10-424-599-24931	Sequence 24931, A	
31	100	22.7	332	20	US-10-425-115-84981	Sequence 84981, A	
32	99.4	22.6	213	20	US-10-425-115-170044	Sequence 170044, A	
33	96.2	21.9	1068	18	US-10-424-599-24932	Sequence 24932, A	
34	92	20.9	1067	20	US-10-425-115-173090	Sequence 173090, A	
35	90.4	20.5	380	14	US-10-062-727-728	Sequence 728, App	
36	88.2	20.0	625	20	US-10-425-115-159906	Sequence 159906, A	
37	87.4	19.9	469	20	US-10-425-115-88983	Sequence 88983, A	
38	85.4	19.4	253	20	US-10-425-115-73082	Sequence 73082, A	
39	83.2	18.9	634	20	US-10-425-115-97131	Sequence 97131, A	
40	79.2	18.0	759	20	US-10-425-115-13402	Sequence 13402, A	
41	79.2	18.0	1923	20	US-10-425-115-149404	Sequence 149404, A	
42	78.8	17.9	1272	19	US-10-437-963-10930	Sequence 10930, A	
43	75.8	17.2	1511	20	US-10-739-930-2432	Sequence 2432, Ap	
44	73	16.6	1014	18	US-10-425-114-27406	Sequence 27406, A	
45	73	16.6	1169	19	US-10-437-963-23832	Sequence 23832, A	

ALIGNMENTS

RESULT 1
US-10-425-114-28279
Sequence 28279, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jinsong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 28279
LENGTH: 892
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB4756-014-F7_FLI
US-10-425-114-28279

Query Match 62.6%; Score 275.6; DB 18; Length: 892;
Best Local Similarity 79.1%; Pred. No. 2e-73;
Matches 348; Conservative 0; Mismatches 86; Indels 6; Gaps 4;
QY 1 CGTCCGCGCGCGCGACTTCGCTTTTCGTCGCCGCGTACGCGCTCCNNTGAGC 60

*Alignment of SEQ/DNA.5
to wheat sequence*

RESULT 5
TAU22442
LOCUS
DEFINITION
Triticum aestivum adenine phosphoribosyltransferase form 1 (APT1)
mRNA, complete cds.
U22442
U22442.1 GI:726304
845 bp mRNA linear PLN 08-NOV-1995
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Triticum aestivum (bread wheat)
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
1 (bases 1 to 845)
Moffatt,B.A., Schnorr,K., Galliard,C., Biget,E. and Laloue,M.
Nucleotide sequence of a wheat cDNA encoding Adenine
Phosphoribosyltransferase (GenBank U22442) (PGR95-030)
Plant Physiol. 108 (4), 1748 (1995)
2 (bases 1 to 845)
Schnorr,K.S., Moffatt,B.A., Biget,E. and Laloue,M.
Direct Submission
Submitted (10-MAR-1995) Kirk Matthew Schnorr, Department of
Biological Chemistry, Institute of Molecular Biology, University of
Copenhagen, Solvgade 83, Copenhagen K, DK 1307, Denmark
Location/Qualifiers
1. 845
/organism="Triticum aestivum"
/mol_type="mRNA"
/strain="Capitol"
/db_xref="taxon:4565"
/tissue_type="Immature seeds"
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1. 845
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48. 593
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594. 845
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845
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ORIGIN
3' UTR
polyA_site

Query Match 28.0%; Score 123.2; DB 8; Length 845;
Best Local Similarity 66.1%; Pred. No. 2.2e-18;
Matches 211; Conservative 0; Mismatches 101; Indels 7; Gaps 4;

QY	77	GCAAGCGAAGGCGAGCGGTGTGGCCATGGCGTNGCTGATGCGCGCTTGCGGNGATCG	136
DB	22	GGGCGGCGAGGGTTCGGCGCGGTTCGATGGCATCC--GACGGCGGTGAGCGGATCG	78
QY	137	NGTCTTCATCCNGGTNATNCCGACTTNCACAAAGCAGGATNATGTTTCAGACATCA	196
DB	79	CGTCCAGCATCCGCGCCATCCCACTTCCCAAGCCAGGATTTGTTTCAGACATCA	138
QY	197	NGANGTGTGATGCCAAGCGGTCGGTGCACACATATACCATTTTGTCAAGCGGT	256
DB	139	CACCTTGCTTCTGATCCGAGGCATTCGTCACACATGACCTCTTGTGAGCGGT	198
QY	257	ACAAGACCAAGNATCACCTTGAAANTAGAGGTTAAAGCTAGAGGANTCANTTCCGA	316
DB	199	ACAAGACCAAGACATACCTAGTGTCT-GGTGTGAAGCCAGAGATTCATTTTGGT	257
QY	317	ACAACCTANNCTTANANNAATGTGCAAAAATNGTENCNATTTAGAGGACNNATNAG	376
DB	258	CTCCCATTTGC-ATTAGCCATAGGTGCAAGTTTGT-TCCAATNAGGAAGCCGAAAAA	314
QY	377	NTGCCANGCNAATGATTT	395
DB	315	TTACTGTGTGAGGTGATAT	333

beq5a-a1522952.rev

TOIG of: a1522952 check: 8094 from: 1 to: 445

PHOSPHORIBOSYLTRANSFERASE 1 ; , mRNA_sequence

ACCESSION	AI522952
VERSION	AI522952.1
	GI:4437087

SOURCE	Glycine max (soybean)
ORGANISM	Glycine max

1 (bases 1 to 445)

TITLE	Public Soybean EST Project
JOURNAL	Unpublished (1999)
COMMENT	Contact: Shoemaker R/Public Soybean EST Project

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. Possible reversed clone: similarity on wrong strand This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)

Seq primer: -40RP from Gibco
High quality sequence stop: 438
POLYA=No.

FEATURES	Location/Qualifiers
source	1. .445

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1. .445
/organism="Glycine max"
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/lab_host="X110-Gold"
/clone_11b="Gm-c1004"
/notes="Vector: pBluescript II XR; Site 1: EcoRI; Site 2:
XhoI; Root cDNA. The mRNA was isolated from entire roots
of 8 day old 'Williams' seedlings which were propagated on
paper towels with distilled water. Stratagene's cDNA
Synthesis Kit (catalog #200401) was used to synthesize the
cDNA. First-strand synthesis was performed with 5-methyl
dCTP, hence the ligated cDNA is hemimethylated.
Stratagene's first-strand synthesis primer was used
(GAGAGAGAGAGAGAGAGAACTAGTCGAG(T)-18). After
second-strand synthesis, the cDNA ends were 'polished'
with clone Pfu DNA polymerase, ligated to EcoRI adapters,
and phosphorylated. The XhoI site within the first-strand
synthesis primer was restricted by digestion with XhoI;
all XhoI sites in the cDNA would be protected by their
hemimethylated status. The cDNA constructs were

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size-fractionated with a 500bp cutoff, using GibcoBRL Life Technologies' cDNA Size Fractionation column. The column eluent was then ligated into Stratagene's pBluescript II XR Predigested vector (pBluescript II SK(+)) that had been digested with EcoRI and XhoI, and phosphorylated). Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts. Blue colonies 9a-15 have been sequenced, and possess putative cDNA inserts. This library was constructed by Dr. Paul Keim & Virginia H. Coryell, Department of Biology, Box5640, Northern Arizona University, Flagstaff, AZ 86011, Phone: 520-523-1078 (Dr. Paul Keim), 520-523-1372 (Virginia H. Coryell), Fax: 520-523-7500, email: paul.keim@nau.edu, virginia.coryell@nau.edu"

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AI522952 Length: 445 September 26, 2005 11:16 Type: N Check: 8094 ...
Initial Score = 26 Optimized Score = 121 Significance = 0.000
Residue Identity = 44% Matches = 134 Mismatches = 137
Gaps = 33 Conservative Substitutions = 0

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ORIGIN

[illegible]